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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/506,079E

DATE: 08/07/2002  
 TIME: 10:05:05

p#17

Input Set : A:\PatentIn Sequence Listing.txt  
 Output Set: N:\CRF3\08072002\I506079E.raw

3 <110> APPLICANT: Doherty, Joni  
 4 Clinton, Gail M.  
 6 <120> TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS  
 8 <130> FILE REFERENCE: 49321-16  
 10 <140> CURRENT APPLICATION NUMBER: US 09/506,079E  
 11 <141> CURRENT FILING DATE: 2000-02-16  
 13 <150> PRIOR APPLICATION NUMBER: US 09/234,208  
 14 <151> PRIOR FILING DATE: 1999-01-20  
 16 <160> NUMBER OF SEQ ID NOS: 10  
 18 <170> SOFTWARE: PatentIn version 3.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 79  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Homo sapiens  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: MISC\_FEATURE  
 27 <222> LOCATION: (2)..(2)  
 28 <223> OTHER INFORMATION: Applicants herein disclose Thr and Ser sequence variants at  
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 32 <220> FEATURE:  
 33 <221> NAME/KEY: MISC\_FEATURE  
 34 <222> LOCATION: (5)..(5)  
 35 <223> OTHER INFORMATION: Applicants herein disclose Leu and Pro sequence variants at  
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 40 <221> NAME/KEY: MISC\_FEATURE  
 41 <222> LOCATION: (6)..(6)  
 42 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at  
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 46 <220> FEATURE:  
 47 <221> NAME/KEY: MISC\_FEATURE  
 48 <222> LOCATION: (16)..(16)  
 49 <223> OTHER INFORMATION: Applicants herein disclose Leu and Gln sequence variants at  
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 53 <220> FEATURE:  
 54 <221> NAME/KEY: MISC\_FEATURE  
 55 <222> LOCATION: (18)..(18)  
 56 <223> OTHER INFORMATION: Applicants herein disclose Met and Leu sequence variants at  
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 57 position

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60 <220> FEATURE:  
61 <221> NAME/KEY: MISC\_FEATURE  
62 <222> LOCATION: (21)..(21)  
63 <223> OTHER INFORMATION: Applicants herein disclose Gly, Asp, Ala and Val sequence  
variant

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64      s at this position
67 <220> FEATURE:
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70 <223> OTHER INFORMATION: Applicants herein disclose Leu and Ile sequence variants at
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76 <222> LOCATION: (54)..(54)
77 <223> OTHER INFORMATION: Applicants herein disclose Pro and Arg sequence variants at
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84 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at
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89 <221> NAME/KEY: MISC_FEATURE
90 <222> LOCATION: (73)..(73)
91 <223> OTHER INFORMATION: Applicants herein disclose Asp and Asn sequence variants at
this
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W--> 97 Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro Xaa
98 1          5          10          15
W--> 101 Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
102          20          25          30
W--> 105 Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
106          35          40          45
W--> 109 Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val Gly Arg Gly Xaa
110          50          55          60
W--> 113 Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg Tyr Glu Gly
114 65          70          75
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118 <211> LENGTH: 419
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
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131 <222> LOCATION: (345)..(345)
132 <223> OTHER INFORMATION: Applicants herein disclose Leu and Pro sequence variants at
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136 <220> FEATURE:

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137 <221> NAME/KEY: MISC\_FEATURE  
138 <222> LOCATION: (346)..(346)

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139 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at
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143 <220> FEATURE:
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146 <223> OTHER INFORMATION: Applicants herein disclose Leu and Gln sequence variants at
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150 <220> FEATURE:
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152 <222> LOCATION: (358)..(358)
153 <223> OTHER INFORMATION: Applicants herein disclose Met and Leu sequence variants at
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157 <220> FEATURE:
158 <221> NAME/KEY: MISC_FEATURE
159 <222> LOCATION: (361)..(361)
160 <223> OTHER INFORMATION: Applicants herein disclose Gly, Asp, Ala and Val sequence
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166 <222> LOCATION: (376)..(376)
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181 <223> OTHER INFORMATION: Applicants herein disclose Asp and Asn sequence variants at
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187 <222> LOCATION: (394)..(394)
188 <223> OTHER INFORMATION: Applicants herein disclose Pro and Arg sequence variants at
this
189     position
192 <400> SEQUENCE: 2
194 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
195 1           5           10           15
198 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys
199           20           25           30
202 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
203           35           40           45
206 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr

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207	50					55				60						
210	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val
211	65					70					75				80	
214	Gln	Gly	Tyr	Val	Leu	Cys	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu

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215          85          90          95
218 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
219          100          105          110
222 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
223          115          120          125
226 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
227          130          135          140
230 Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
231 145          150          155          160
234 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
235          165          170          175
238 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
239          180          185          190
242 His Pro Cys Ser Pro Cys Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
243          195          200          205
246 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
247          210          215          220
250 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
251 225          230          235          240
254 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
255          245          250          255
258 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
259          260          265          270
262 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg
263          275          280          285
266 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu
267          290          295          300
270 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
271 305          310          315          320
274 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
275          325          330          335
W--> 278 Pro Cys Ala Arg Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val
279          340          345          350
W--> 282 Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser
283          355          360          365
W--> 286 Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro
287          370          375          380
W--> 290 Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
291 385          390          395          400
W--> 294 Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg
295          405          410          415
298 Tyr Glu Gly
302 <210> SEQ ID NO: 3
303 <211> LENGTH: 19
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: HER-2-specific oligonucleotide primer
310 <400> SEQUENCE: 3

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314 <210> SEQ ID NO: 4
315 <211> LENGTH: 22
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
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322 <400> SEQUENCE: 4
323 tccggcagaa atgccaggct cc 22
326 <210> SEQ ID NO: 5
327 <211> LENGTH: 22
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: HER-2 cDNA-specific oligonucleotide primer
334 <400> SEQUENCE: 5
335 aacacagcgg tgtgagaagt gc 22
338 <210> SEQ ID NO: 6
339 <211> LENGTH: 21
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: HER-2 ECDIIIa-region-specific oligonucleotide primer
346 <400> SEQUENCE: 6
347 ataccgggac aggtcaacag c 21
350 <210> SEQ ID NO: 7
351 <211> LENGTH: 20
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial Sequence
355 <220> FEATURE:
356 <223> OTHER INFORMATION: HER-2 ECDIIIa-region-specific oligonucleotide primer
358 <400> SEQUENCE: 7
359 tctgggtacc cactcactgc 20
362 <210> SEQ ID NO: 8
363 <211> LENGTH: 22
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial Sequence
367 <220> FEATURE:
368 <223> OTHER INFORMATION: HER-2 exon-specific oligonucleotide primer
370 <400> SEQUENCE: 8
371 ttcacactgg cacgtccaga cc 22
374 <210> SEQ ID NO: 9
375 <211> LENGTH: 27
376 <212> TYPE: DNA
377 <213> ORGANISM: Artificial Sequence
379 <220> FEATURE:
380 <223> OTHER INFORMATION: HER-2 cDNA-specific oligonucleotide primer
382 <400> SEQUENCE: 9
383 gcacgatcc atagcagact gaggagg 27

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/506,079E

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Input Set : A:\PatentIn Sequence Listing.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,5,6,16,18,21,36,54,64,73

Seq#:2; Xaa Pos. 342,345,346,356,358,361,376,394,404,413

Seq#:10; N Pos. 62

Seq#:10; Xaa Pos. 2,5,6,16,18,21,36,54,64,73